

WEST Search History

DATE: Wednesday, October 11, 2006

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L7	L5 and L3	6
<input type="checkbox"/>	L6	L4 and L3	7
<input type="checkbox"/>	L5	Quanz-M\$.in.	29
<input type="checkbox"/>	L4	Buttcher-V\$.in.	14
<input type="checkbox"/>	L3	L1 and L2	35
<input type="checkbox"/>	L2	branching adj enzyme	2611
<input type="checkbox"/>	L1	neisseria	8491

END OF SEARCH HISTORY

FILE 'AGRICOLA, BIOSIS, CAPLUS' ENTERED AT 15:22:51 ON 11 OCT 2006

L1	26961 S NEISSERIA
L2	1784 S BRANCHING ENZYME
L3	5 S L1 AND L2
L4	9 S BUTTCHER V?/AU
L5	21 S QUANZ M?/AU
L6	4 S L3 AND L5
L7	3 S L3 AND L4

SCORE Search Results Details for Application 10705195-1.rgc

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This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-1.rgc
[start](#)

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OM nucleic - nucleic search, using sw model

Run on: August 22, 2006, 19:21:51 ; Search time 13588 Seconds
(without alignments)
11647.768 Million cell updates/sec

Title: US-10-705-195-1
Perfect score: 2475
Sequence: 1 actgtatgccgtgcagctgg.....taaagcggcaccatactgcc 2475

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
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8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2475	100.0	2475	2	BD236814	BD236814 Nucleic a
2	2475	100.0	2475	2	AR337816	AR337816 Sequence
3	2475	100.0	2475	2	AR479077	AR479077 Sequence
4	2475	100.0	2475	2	AX055494	AX055494 Sequence
5	2475	100.0	2475	15	AF102867	AF102867 Neisseria
6	941.6	38.0	2307	2	AR387231	AR387231 Sequence
7	894.6	36.1	2520	15	AF434710	AF434710 Pectobact
c 8	877.8	35.5	110000	15	AE017220_36	Continuation (37 o
c 9	876.2	35.4	110000	15	CP000026_34	Continuation (35 o
c 10	873	35.3	23506	15	AE008863	AE008863 Salmonell
11	871.4	35.2	110000	15	AE014613_41	Continuation (42 o
12	871.4	35.2	265050	15	AL627281	AL627281 Salmonell
c 13	858.8	34.7	110000	15	AE014075_39	Continuation (40 o
c 14	858.8	34.7	110000	15	AE014075_40	Continuation (41 o
c 15	849.2	34.3	110000	15	CP000038_38	Continuation (39 o
c 16	846	34.2	110000	15	AE005174_43	Continuation (44 o
c 17	846	34.2	110000	15	U00096_35	Continuation (36 o
18	846	34.2	110000	15	AP009048_40	Continuation (41 o
c 19	846	34.2	110000	15	BA000007_42	Continuation (43 o
c 20	846	34.2	110000	15	CP000036_34	Continuation (35 o
c 21	845	34.1	72438	15	ECOUW67_3	Continuation (4 of
22	844.4	34.1	2361	2	BD071178	BD071178 Plant lik
23	844.4	34.1	2559	15	ECOGLGBA	M13751 Escherichia
c 24	841.2	34.0	110000	15	AE005674_35	Continuation (36 o
25	841.2	34.0	110000	15	AE014073_42	Continuation (43 o
c 26	839.6	33.9	110000	15	CP000034_33	Continuation (34 o
c 27	837.4	33.8	110000	15	BX950851_46	Continuation (47 o
c 28	789.8	31.9	110000	15	CP000057_16	Continuation (17 o
c 29	789.8	31.9	349980	2	CQ873160	CQ873160 Sequence
c 30	779.8	31.5	6306	2	CQ872897	CQ872897 Sequence
31	773.8	31.3	2055	2	CS221362	CS221362 Sequence
32	768	31.0	12144	15	AE013993	AE013993 Yersinia
c 33	768	31.0	199050	15	AJ414159	AJ414159 Yersinia
c 34	768	31.0	294253	15	AE017139	AE017139 Yersinia
c 35	763.2	30.8	110000	15	BX936398_44	Continuation (45 o
36	759.6	30.7	110000	2	BD426631_14	Continuation (15 o
37	759.6	30.7	110000	2	AR274513_14	Continuation (15 o
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39	759.6	30.7	110000	15	L42023_14	Continuation (15 o
40	758.2	30.6	12519	15	AE006089	AE006089 Pasteurel
c 41	752	30.4	110000	15	AE016827_11	Continuation (12 o
c 42	731.8	29.6	110000	15	AP007255_33	Continuation (34 o
c 43	704.6	28.5	110000	15	CP000250_21	Continuation (22 o
c 44	704.4	28.5	110000	15	BX936398_45	Continuation (46 o
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ALIGNMENTS

RESULT 1

BD236814

LOCUS BD236814 2475 bp DNA linear PAT 17-JUL-2003

DEFINITION Nucleic acid molecule encoding branching enzyme from Neisseria
bacteria and process for producing alpha-1,6-branched
alpha-1,4-glucane.

ACCESSION BD236814
 VERSION BD236814.1 GI:33046584
 KEYWORDS JP 2002527068-A/1.
 SOURCE Bergeriella denitrificans
 ORGANISM Bergeriella denitrificans
 Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 Neisseriaceae; Bergeriella.
 REFERENCE 1 (bases 1 to 2475)
 AUTHORS Buttcher,V. and Quanz,M.
 TITLE Nucleic acid molecule encoding branching enzyme from Neisseria
 bacteria and process for producing alpha-1,6-branched
 JOURNAL Patent: JP 2002527068-A 1 27-AUG-2002;
 PLANTTEC BIOTECHNOLOGIE GMBH FORSCHUNG UND ENTWICKLUNG, MAX PLANCK
 GESELLSCHAFT ZUR FOERDERUNG DER WISSENSCHAFTEN EV
 COMMENT OS Neisseria denitrificans
 PN JP 2002527068-A/1
 PD 27-AUG-2002
 PF 08-OCT-1999 JP 2000576030
 PR 09-OCT-1998 DE 198 46 635.8,27-MAY-1999 DE 199 24 342.5 PI
 VOLKER BUTTCHER,MARTIN QUANZ
 PC C12N15/09,A01H5/00,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/
 PC 10,C12N9/10,
 PC C12P19/04,C12N15/00,C12N5/00
 CC Nucleic acid molecule encoding branching
 enzyme from Neisseria
 CC bacteria
 CC and process for producing alpha-1,6-branched alpha-1,4-glucane
 FH Key Location/Qualifiers
 FT CDS (170)..(2458).
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 ORIGIN

Query Match 100.0%; Score 2475; DB 2; Length 2475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG	60
Db	1	ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG	60
Qy	61	CGTGGCCGAAGGCTATCCGAAGTGGGCGCGCAAATGCCGCAGCCTCTGGAAGCCTTTGC	120
Db	61	CGTGGCCGAAGGCTATCCGAAGTGGGCGCGCAAATGCCGCAGCCTCTGGAAGCCTTTGC	120
Qy	121	CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA	180
Db	121	CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA	180
Qy	181	CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT	240
Db	181	CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT	240
Qy	241	GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA	300
Db	241	GTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGTGTCAACGACGA	300
Qy	301	ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATCATCGACCGCCA	360

Db	301	 ACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATCATCGACCGCCA	360
Qy	361	CACAGGCGCAGTCATCATGCCGTCTGAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT	420
Db	361	 CACAGGCGCAGTCATCATGCCGTCTGAAAAATCGACGAGCGCGGCCTGTTTGCCGCCGT	420
Qy	421	ATTGCCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC	480
Db	421	 ATTGCCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAGGGCGAAGCCGC	480
Qy	481	CGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACCGATGCCTGGCT	540
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Db	1021	 GGTGAACATATGTAAAAGACATGGGCTTCACCCACATCGAGCTGCTGCCCTTGTCGAATA	1080
Qy	1081	TCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGCCTGTATGCACCGACAGCCGCTT	1140
Db	1081	 TCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGCCTGTATGCACCGACAGCCGCTT	1140
Qy	1141	CGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCCGCCACGCCCGGCATCAGCGT	1200
Db	1141	 CGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCCGCCACGCCCGGCATCAGCGT	1200
Qy	1201	GATTCTCGACTGGGTAGCGGGGCACTTCCCCACCGACGACCACGGCCTCAACACCTTCGA	1260

SCORE Search Results Details for Application 107 Search Result us-10-705-195-1.rng.

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OM nucleic - nucleic search, using sw model

Run on: August 22, 2006, 19:15:26 ; Search time 1535 Seconds
(without alignments)
11241.899 Million cell updates/sec

Title: US-10-705-195-1
Perfect score: 2475
Sequence: 1 actgtatgccgtgcagctgg.....taaagcggcaccatactgcc 2475

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	2475	100.0	2475	3	AAA11731	Aaa11731 N. denitr
2	941.6	38.0	2307	11	ACH98165	Ach98165 Klebsiell
3	846	34.2	2187	13	ADT48837	Adt48837 Bacterial
4	844.4	34.1	2361	2	AAV70952	Aav70952 DNA seque
c 5	789.8	31.9	349980	13	ADT05737	Adt05737 Haemophil
c 6	779.8	31.5	6306	13	ADT05474	Adt05474 Haemophil
7	759.6	30.7	110000	2	AAT42063_14	Continuation (15 o
8	757.4	30.6	2193	8	ACA34445	Aca34445 Prokaryot
9	690.2	27.9	2151	13	ADS55782	Ads55782 Bacterial
10	680.6	27.5	2164	13	ADT46098	Adt46098 Bacterial
11	678.6	27.4	2199	13	ADS14563	Ads14563 Pseudomon
12	670.6	27.1	2472	11	ABD09593	Abd09593 Pseudomon
13	663.6	26.8	2154	13	ADS63589	Ads63589 Bacterial
14	663	26.8	2160	13	ADS63965	Ads63965 Bacterial
15	663	26.8	2160	13	ADT41565	Adt41565 Bacterial
16	657	26.5	2079	5	AAS88840	Aas88840 DNA encod
17	647.8	26.2	2331	6	ABQ90257	Abq90257 M. capsul
18	647.4	26.2	2214	13	ADS60312	Ads60312 Bacterial
19	644.6	26.0	2163	13	ADS62134	Ads62134 Bacterial
20	627.4	25.3	2142	13	ADS63957	Ads63957 Bacterial
21	627.4	25.3	2142	13	ADS64325	Ads64325 Bacterial
22	627.4	25.3	2142	13	ADS63584	Ads63584 Bacterial
23	617.2	24.9	2172	14	ACL68441	Acl68441 M. xanthu
24	617.2	24.9	2205	13	ADT44556	Adt44556 Bacterial
c 25	617.2	24.9	11276	14	ACL64571	Acl64571 M. xanthu
26	593.6	24.0	2148	13	ADT46962	Adt46962 Bacterial
27	567	22.9	2193	8	ACF39411	Acf39411 Mycobacte
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c 29	554.4	22.4	110000	4	AAI99683_14	Continuation (15 o
30	546.8	22.1	2118	13	ADS45889	Ads45889 Bacterial
31	546	22.1	1884	13	ADS57041	Ads57041 Bacterial
32	546	22.1	2034	10	ADG18862	Adg18862 DNA encod
33	537.6	21.7	2178	13	ADT44839	Adt44839 Bacterial
34	521.2	21.1	1434	5	AAS93435	Aas93435 DNA encod
c 35	521.2	21.1	1434	5	AAS93857	Aas93857 DNA encod
36	512.2	20.7	2157	13	ADS58032	Ads58032 Bacterial
37	510.2	20.6	349980	6	ABQ81846	Abq81846 Bifidobac
38	510.2	20.6	349980	6	ABQ81847	Abq81847 Bifidobac
39	504.8	20.4	22934	4	AAS59613	Aas59613 Propionib
40	504.8	20.4	22934	8	ACF64542	Acf64542 Propionib
c 41	503.6	20.3	1701	11	ABD09505	Abd09505 Pseudomon
42	471.4	19.0	2268	13	ADT46200	Adt46200 Bacterial
43	457	18.5	1866	3	AAC61606	Aac61606 DNA encod
44	457	18.5	1866	12	ADH01235	Adh01235 cDNA enco
45	443.4	17.9	2313	13	ADS48037	Ads48037 Bacterial

ALIGNMENTS

RESULT 1

AAA11731

ID AAA11731 standard; DNA; 2475 BP.

XX

AC AAA11731;

XX

DT 21-JUL-2000 (first entry)
 XX
 DE N. denitrificans alpha-1,6-branched alpha-1,4 glucan DNA.
 XX
 KW Alpha-1,6-branched alpha-1,4-glucan; branching enzyme; binder; carrier;
 KW transgenic plant; flavor; perfume; packaging material; papermaking;
 KW ultra-violet light adsorber; starch; textile; wetting agent; ds.
 XX
 OS Neisseria denitrificans.
 XX
 FH Key Location/Qualifiers
 FT CDS 170. .2458
 FT /*tag= a
 FT /product= "alpha-1,6-branched alpha-1,4-glucan"
 XX
 PN WO200022140-A1.
 XX
 PD 20-APR-2000.
 XX
 PF 08-OCT-1999; 99WO-EP007562.
 XX
 PR 09-OCT-1998; 98DE-01046635.
 PR 27-MAY-1999; 99DE-01024342.
 XX
 PA (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.
 PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 XX
 PI Buettcher V, Quanz M;
 XX
 DR WPI; 2000-317992/27.
 DR P-PSDB; AAW90977.
 XX
 PT New nucleic acid encoding a branching enzyme, useful for in vitro
 PT synthesis of branched glucans and to prepare transgenic plants producing
 PT modified starch.
 XX
 PS Claim 1b; Page 93-96; 115pp; German.
 XX
 CC This invention describes a novel nucleic acid (I) isolated from Neisseria
 CC which encodes a branching enzyme (II). (I) is used for recombinant
 CC production of (II) subsequently used in the in vitro production of alpha-
 CC 1,6-branched alpha-1,4-glucans. It is also used to prepare transgenic
 CC plants that produce starches with modified properties. (III) are used as
 CC binders for tablets, carriers for pharmaceuticals, flavors and perfumes
 CC and powdered additives, packaging materials, ultra-violet light adsorbers
 CC in sunscreens and also for any of the usual applications of starch in
 CC foods, papermaking, as textile size, in soil stabilization, as wetting
 CC agent for agricultural chemicals, as polymer additives etc. Fragments of
 CC (I) are useful as PCR primers and antisense molecules or ribozymes for
 CC inhibiting expression of (I), and the regulatory region of (II) can be
 CC used to control expression of heterologous sequences in host cells. (I)
 CC provides an inexpensive method for producing alpha-1,6-branched alpha-1,4
 CC -glucans (III), producing products that can be tailored for particular
 CC applications, particularly by controlling the degree of branching. Starch
 CC from transgenic plants has increased gel strength; reduced phosphate
 CC content; reduced peak viscosity; lower pasting temperature and granule
 CC size and/or altered sidechain distribution. This sequence encodes an
 CC alpha-1,6-branched alpha-1,4-glucan isolated from Neisseria denitrificans
 CC which is described in the method of the invention
 XX
 SQ Sequence 2475 BP; 560 A; 827 C; 674 G; 414 T; 0 U; 0 Other;

Query Match 100.0%; Score 2475; DB 3; Length 2475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	ACTGTATGCCGTGCAGCTGGAAAACCTGCTGGGCGTACGCGACAACCTCAATATTCCCGG	60
Qy	61	CGTGGCCGAAGGCTATCCGAACCTGGGCGCGCAAAATGCCGAGCCTCTGGAAGCCTTTGC	120
Db	61	CGTGGCCGAAGGCTATCCGAACCTGGGCGCGCAAAATGCCGAGCCTCTGGAAGCCTTTGC	120
Qy	121	CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA	180
Db	121	CCGCCACCCGCAAATGGGCAAGCAGCTTGCCATGATGGGAGACATCCGCATGAACCGAAA	180
Qy	181	CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT	240
Db	181	CCGCCATATCCGACGCGGCTACCACCCGGAAGCCGAGAACGCCAAATCATCGACAGCCT	240
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Qy	541	GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTGCCGAAAT	600
Db	541	GCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACATTTGCCGAAAT	600
Qy	601	GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGGGTATCGGT	660
Db	601	GGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGGGGTATCGGT	660
Qy	661	CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA	720
Db	661	CATCGGCGAATTCAACGGCTGGGACAGCCGCCCATGCCATGCGTCCGCACACAGGCAA	720
Qy	721	CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT	780
Db	721	CGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTATAAATTCTCCGT	780
Qy	781	ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTGCGCGCGGAGCT	840
Db	781	ACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGACCCCTACGCATTGCGCGCGGAGCT	840

SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-1.rni.

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This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-1.rni.
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2006, 19:27:21 ; Search time 466 Seconds
 (without alignments)
 9937.756 Million cell updates/sec

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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	IDB	ID	Description

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4	759.6	30.7	1830121	3	US-09-557-884-1	Sequence 1, Appli
5	759.6	30.7	1830121	3	US-09-643-990A-1	Sequence 1, Appli
6	759.6	30.7	1830121	3	US-10-158-865-1	Sequence 1, Appli
7	670.6	27.1	2472	3	US-09-252-991A-8197	Sequence 8197, Ap
8	617.2	24.9	2172	3	US-09-902-540-4904	Sequence 4904, Ap
c 9	617.2	24.9	11276	3	US-09-902-540-1034	Sequence 1034, Ap
c 10	567	22.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 11	554.4	22.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 12	503.6	20.3	1701	3	US-09-252-991A-8109	Sequence 8109, Ap
13	457	18.5	1866	3	US-09-537-120-1	Sequence 1, Appli
14	370	14.9	1308	3	US-09-252-991A-8131	Sequence 8131, Ap
15	324.2	13.1	2426	3	US-08-528-026C-3	Sequence 3, Appli
16	314.6	12.7	36470	3	US-08-311-731A-123	Sequence 123, App
c 17	314.6	12.7	1230025	3	US-09-198-452A-1	Sequence 1, Appli
c 18	314.6	12.7	1230230	3	US-09-438-185A-1	Sequence 1, Appli
19	277.6	11.2	1877	5	US-09-974-300-653	Sequence 653, App
20	201.8	8.2	1929	3	US-09-583-110-1148	Sequence 1148, Ap
21	201.8	8.2	1956	3	US-09-107-433-242	Sequence 242, App
c 22	186.6	7.5	11384	3	US-08-961-527-45	Sequence 45, Appl
c 23	167	6.7	702	3	US-09-252-991A-8108	Sequence 8108, Ap
24	161.4	6.5	807	3	US-09-634-238-168	Sequence 168, App
25	157	6.3	976	3	US-08-961-083-79	Sequence 79, Appl
26	157	6.3	976	3	US-09-536-784-79	Sequence 79, Appl
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28	157	6.3	976	3	US-09-765-272A-79	Sequence 79, Appl
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33	100.6	4.1	5402	3	US-09-221-017B-194	Sequence 194, App
34	93.4	3.8	461	3	US-09-634-238-167	Sequence 167, App
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42	69.4	2.8	2307	3	US-09-786-480B-1	Sequence 1, Appli
43	67.8	2.7	2554	5	US-10-162-948-1	Sequence 1, Appli
44	67.8	2.7	2853	3	US-09-609-040-3	Sequence 3, Appli
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ALIGNMENTS

RESULT 1

US-09-579-365-1

; Sequence 1, Application US/09579365

; Patent No. 6566585

; GENERAL INFORMATION:

; APPLICANT: Martin QUANZ

; TITLE OF INVENTION: GENETICALLY MODIFIED PLANT CELLS AND PLANTS WITH AN

; TITLE OF INVENTION: INCREASED ACTIVITY OF AN AMYLOSUCRASE PROTEIN AND A

; TITLE OF INVENTION: BRANCHING ENZYME

; FILE REFERENCE: 0147-0200P

; CURRENT APPLICATION NUMBER: US/09/579,365

; CURRENT FILING DATE: 2000-05-25
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 2475
 ; TYPE: DNA
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 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (170)..(2458)
 US-09-579-365-1

Query Match 100.0%; Score 2475; DB 3; Length 2475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	1561	CGCCGGCTCGTTTGCCGAAGAATCGACTTCCTTTGCCGACGTAACCCGCGAAGCCGGCCT	1620

SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-1.rni.

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This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-1.rni.
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 (without alignments)
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Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	941.6	38.0	2307	3	US-09-489-039A-3960	Sequence 3960, Ap
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	5	759.6	30.7	1830121	3	US-09-643-990A-1	Sequence 1, Appli
	6	759.6	30.7	1830121	3	US-10-158-865-1	Sequence 1, Appli
	7	670.6	27.1	2472	3	US-09-252-991A-8197	Sequence 8197, Ap
	8	617.2	24.9	2172	3	US-09-902-540-4904	Sequence 4904, Ap
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c	10	567	22.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	11	554.4	22.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	12	503.6	20.3	1701	3	US-09-252-991A-8109	Sequence 8109, Ap
	13	457	18.5	1866	3	US-09-537-120-1	Sequence 1, Appli
	14	370	14.9	1308	3	US-09-252-991A-8131	Sequence 8131, Ap
	15	324.2	13.1	2426	3	US-08-528-026C-3	Sequence 3, Appli
	16	314.6	12.7	36470	3	US-08-311-731A-123	Sequence 123, App
c	17	314.6	12.7	1230025	3	US-09-198-452A-1	Sequence 1, Appli
c	18	314.6	12.7	1230230	3	US-09-438-185A-1	Sequence 1, Appli
	19	277.6	11.2	1877	5	US-09-974-300-653	Sequence 653, App
	20	201.8	8.2	1929	3	US-09-583-110-1148	Sequence 1148, Ap
	21	201.8	8.2	1956	3	US-09-107-433-242	Sequence 242, App
c	22	186.6	7.5	11384	3	US-08-961-527-45	Sequence 45, Appl
c	23	167	6.7	702	3	US-09-252-991A-8108	Sequence 8108, Ap
	24	161.4	6.5	807	3	US-09-634-238-168	Sequence 168, App
	25	157	6.3	976	3	US-08-961-083-79	Sequence 79, Appl
	26	157	6.3	976	3	US-09-536-784-79	Sequence 79, Appl
	27	157	6.3	976	3	US-09-765-271-79	Sequence 79, Appl
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	33	100.6	4.1	5402	3	US-09-221-017B-194	Sequence 194, App
	34	93.4	3.8	461	3	US-09-634-238-167	Sequence 167, App
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c	36	87.6	3.5	4125	3	US-09-252-991A-8065	Sequence 8065, Ap
	37	80.4	3.2	1896	3	US-09-902-540-6849	Sequence 6849, Ap
c	38	80.4	3.2	5043	3	US-09-902-540-574	Sequence 574, App
c	39	78.8	3.2	1770	3	US-09-252-991A-8263	Sequence 8263, Ap
	40	78.8	3.2	1947	3	US-09-252-991A-8057	Sequence 8057, Ap
	41	73.8	3.0	2955	4	US-09-880-107-2148	Sequence 2148, Ap
	42	69.4	2.8	2307	3	US-09-786-480B-1	Sequence 1, Appli
	43	67.8	2.7	2554	5	US-10-162-948-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1

US-09-579-365-1

; Sequence 1, Application US/09579365

; Patent No. 6566585

; GENERAL INFORMATION:

; APPLICANT: Martin QUANZ

; TITLE OF INVENTION: GENETICALLY MODIFIED PLANT CELLS AND PLANTS WITH AN

; TITLE OF INVENTION: INCREASED ACTIVITY OF AN AMYLOSUCRASE PROTEIN AND A

; TITLE OF INVENTION: BRANCHING ENZYME

; FILE REFERENCE: 0147-0200P

; CURRENT APPLICATION NUMBER: US/09/579,365

; CURRENT FILING DATE: 2000-05-25
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 ; SEQ ID NO 1
 ; LENGTH: 2475
 ; TYPE: DNA
 ; ORGANISM: Neisseria denitrificans
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (170)..(2458)
 US-09-579-365-1

Query Match 100.0%; Score 2475; DB.3; Length 2475;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2475; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-1.rn

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This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-1.rn.pbm.

[start](#)

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

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	7	759.6	30.7	1830121	9	US-10-158-865-1	Sequence 1, Appli
	8	759.6	30.7	1830121	10	US-10-981-687-1	Sequence 1, Appli
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US-10-705-195-1

; Sequence 1, Application US/10705195

; Publication No. US20040110254A1

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; GENERAL INFORMATION:
; APPLICANT: BUTTCHER, Volker et al.
; TITLE OF INVENTION: Method for producing alpha-1, 6-branched alpha-1, 4-glucans fro
; FILE REFERENCE: 0147-0253P
; CURRENT APPLICATION NUMBER: US/10/705,195
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US 09/807,063
; PRIOR FILING DATE: 2001-04-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Neisseria denitrificans
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (170)..(2458)
US-10-705-195-1
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SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-1.rnpbn

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7	95	3.8	641	8	US-11-266-748A-134052	Sequence 134052,
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; Sequence 17, Application US/11275569

; Publication No. US20060160192A1

; GENERAL INFORMATION:

; APPLICANT: Ajinomoto Co., Inc.

; TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACID USING BACTERIUM OF THE

; TITLE OF INVENTION: ENTEROBACTERIACEAE FAMILY HAVING PATHWAY OF GLYCOGEN BIOSYNTHETIC

; FILE REFERENCE: C440-C5323

; CURRENT APPLICATION NUMBER: US/11/275,569


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; CURRENT FILING DATE: 2006-01-17
; PRIOR APPLICATION NUMBER: RU2005101110
; PRIOR FILING DATE: 2005-01-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
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; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2187)
US-11-275-569-17
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Best Local Similarity 62.6%; Pred. No. 5.9e-206;
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Qy      278 GGGCGGCATCGTGTCAACGACGAACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCAC 337
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Db      76 GGAATGCATAAAACCACGCGGGACTGGAAG---TCCGTGCCCTTTTACCCGACGCTACC 132

Qy      338 CACATCGACATCATCGACCGCCACACAGGCGCAGTCATCATGCCGTCTGAAAAAATCGAC 397
      | | | | | | | | | | | | | | | | | | | | | |
Db      133 GATGTGTGGGTGATTGAACCGAAAACCGGGCGCAAACCTCGCAAACCTGGAGTGTCTCGAC 192

Qy      398 GAGCGCGGCCTGTTTGCCGCCGTATTGCCCGAACACGCGCCCGACTACGCCCTGCTGGTG 457
      || || | | | | | | | | | | | | | | | | | | | |
Db      193 TCACGGGGATTCTTTAGCGGCGTCATTCCGCGACGTAAGAATTTTTTCCGCTATCAGTTG 252

Qy      458 ACATACCACGAGGGCGAAGCCGCCGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCG 517
      | | | | | | | | | | | | | | | | | | | | | |
Db      253 GCTGTTGTCTGGCATGGTCAGCAAACCTGATTGATGATCCTTACCGTTTTGGTCCGCTA 312

Qy      518 CTGCAACATAACCGATGCCTGGCTGCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACG 577
      | || | | | | | | | | | | | | | | | | | | | | |
Db      313 ATCCAGGAAATGGATGCCTGGCTATTATCTGAAGGTACTCACCTGCGCCCGTATGAAACC 372

Qy      578 CTGGGCGCACATTTCCGCCAAATGGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCG 637
      | | | | | | | | | | | | | | | | | | | | | |
Db      373 TTAGGCGCGCATGCAGATACTATGGATGGCGTCACAGGTACGCGTTTCTCTGTCTGGGCT 432

Qy      638 CCCAACGCGCGCGGGGTATCGGTCATCGGCGAATTCAACGGCTGGGACAGCCGCCGCCAT 697
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Db      433 CCAAACGCCCCTCGGGTCTCGGTGGTTGGGCAATTCAACTACTGGGACGGTCGCCGTCAC 492

Qy      698 GCCATGCGTCCGCACACAGGCAACGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTC 757
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Db      493 CCGATGCGCCTGCGTAAAGAGAGCGGCATCTGGGAACTGTTTATCCCTGGGGCGCATAAC 552

Qy      758 AACGCGCTGTATAAATTCTCCGTACTCGATGCCAACGGCAACATCCGCGAAAAAGCCGAC 817
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Db      553 GGTCAGCTCTATAAATACGAGATGATTGATGCCAATGGCAACTTGCGTCTGAAGTCCGAC 612

Qy      818 CCCTACGCATTTCGGCGCGGAGCTGCGCCCGACCACCGCATCCGTGGTGCGCGGCTTGCCG 877
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Db	673	GAAAAGGTTGTACAGACTGAAGAGCGCAAAAAGCGAATCAGTTTGATGCGCCAATCTCT	732
Qy	938	ATTTACGAAGTCCATCTCGGCTCGTGGCGGCGCAATCCCGAAAACAATACTGGCTCACC	997
Db	733	ATTTATGAAGTTCACCTGGGTTCTCGGCTCGCCACACCGACAACAATTTCTGGTTGAGC	792
Qy	998	TACACGCAGCTGGCCGACGAATTGGTGAATATGTAAAAGACATGGGCTTCACCCACATC	1057
Db	793	TACCGCGAGCTGGCCGATCAACTGGTGCCTTATGCTAAATGGATGGGCTTTACCCACCTC	852
Qy	1058	GAGCTGCTGCCCTTGTCCGAATATCCGTTTCGACGGCTCATGGGGCTACCAAGCCACCGGC	1117
Db	853	GAATACTGCCCATTAAACGAGCATCCCTTCGATGGCAGTTGGGGTTATCAGCCAACCGGC	912
Qy	1118	CTGTATGCACCGACCAGCCGCTTCGGCTCGCCCGATGAGCTGAAAGCCCTGATTGACGCC	1177
Db	913	CTGTATGCGCCAACCCGCCGTTTTGGTACTCGCGACGACTTCCGTTATTTTCATTGATGCC	972
Qy	1178	GCCACGCGCCCGGCATCAGCGTGATTCTCGACTGGGTAGCGGGGCACTTCCCCACCGAC	1237
Db	973	GCACACGCAGCTGGTCTGAACGTGATTCTCGACTGGGTGCCAGGCCACTTCCCGACTGAT	1032
Qy	1238	GACCACGGCCTCAACACCTTCGACGGCACGGCGCTTTACGAACACGCCGACCCGCGCGAA	1297
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Qy	1298	GGCTACCATCAGGATTGGAACACGCTGATTTACAATTCGGCCGCAACGAAGTCAAAAAC	1357
Db	1093	GGCTATCATCAGGACTGGAACACGCTGATCTACAATATGGTCGCCGTGAAGTCAGTAA	1152
Qy	1358	TTCTGTCAGGGCAACGCGCTCTACTGGATTGAGCGTTTTCGGCTTCGACGGCATCCGCGTG	1417
Db	1153	TTCTCGTCGGTAACGCGCTTTACTGGATTGAACGTTTTGGTATTGATGCGCTGCGCGTC	1212
Qy	1418	GACGCCGTGGCCTCGATGATTTACCGCAACTACTCGCGCAAAGACGGCGAGTGGATTCCC	1477
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Qy	1478	AACCGCTACGGCGGCAGCGAAAATCTGGAAGCCATCGCCTTTTTGCGCCAAACCAATGCC	1537
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Qy	1538	GTCTTAAAAAGCGAAACACCCGGCGCCGGCTCGTTTTGCCGAAGAATCGACTTCCTTTGCC	1597
Db	1333	ATTCTTGGTGAGCAGTTTCCGGTGCGGTGACAATGGCTGAGGAGTCTACCGATTTCCT	1392
Qy	1598	GACGTAACCCG-----CGAAGCCGGCCTGAACTTCGATTTCAAATGGAATATGGGC	1648
Db	1393	GGCGTTTCTCGTCCGAGGATATGGGCGGTCTGGGCTTCTGGTACAAGTGAACCTCGGC	1452
Qy	1649	TGGATGAACGACACCCTGCGCTATATGCAGGAAGACCCCGTCCACCGCAAATACCACCAC	1708
Db	1453	TGGATGCATGACACCCTGGACTACATGAAGCTCGACCCGGTTTATCGTCAGTATCATCAC	1512
Qy	1709	GGCAAAATGACATTCCGGCATGATGTACCAATACAGCGAAAACCTTCGTTCTGCCCTGTCTG	1768
Db	1513	GATAAACTGACCTTCGGGATTCTCTACAATACTGAAAACCTTCGTCCTGCCGTTGTCTG	1572

SCORE Search Results Details for Application 2.p2r

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This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-1... [start](#)

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2006, 19:34:08 ; Search time 11195 Seconds
(without alignments)
6528.977 Million cell updates/sec

Title: US-10-705-195-2
Perfect score: 4112
Sequence: 1 MNRNRHIRRGYHPEAGERQI.....QTALRADKQPAVKDKQAKAK 762

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	4112	100.0	2475	2	AR479077	AR479077 Sequence
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	5	4112	100.0	2475	15	AF102867	AF102867 Neisseria
c	6	2570	62.5	110000	15	AE016827_11	Continuation (12 o
	7	2568.5	62.5	12519	15	AE006089	AE006089 Pasteurel
	8	2533	61.6	2307	2	AR387231	AR387231 Sequence
c	9	2531	61.6	110000	15	CP000057_16	Continuation (17 o
c	10	2531	61.6	349980	2	CQ873160	CQ873160 Sequence
	11	2526	61.4	110000	2	BD426631_14	Continuation (15 o
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	13	2526	61.4	110000	2	AR632719_14	Continuation (15 o
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c	15	2481.5	60.3	6306	2	CQ872897	CQ872897 Sequence
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	17	2472.5	60.1	110000	15	AE014613_41	Continuation (42 o
	18	2472.5	60.1	265050	15	AL627281	AL627281 Salmonell
c	19	2471.5	60.1	23506	15	AE008863	AE008863 Salmonell
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	27	2462.5	59.9	2361	2	BD071178	BD071178 Plant lik
	28	2462.5	59.9	2559	15	ECOGLGBA	M13751 Escherichia
c	29	2462.5	59.9	110000	15	U00096_35	Continuation (36 o
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c	32	2457.5	59.8	72438	15	ECOUW67_3	Continuation (4 of
	33	2456.5	59.7	2055	2	CS221362	CS221362 Sequence
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c	35	2454.5	59.7	110000	15	CP000036_34	Continuation (35 o
	36	2438	59.3	12144	15	AE013993	AE013993 Yersinia
c	37	2438	59.3	110000	15	BX936398_44	Continuation (45 o
c	38	2438	59.3	199050	15	AJ414159	AJ414159 Yersinia
c	39	2438	59.3	294253	15	AE017139	AE017139 Yersinia
c	40	2435.5	59.2	110000	15	BX950851_46	Continuation (47 o
	41	2430	59.1	2520	15	AF434710	AF434710 Pectobact

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	43	2068.5	50.3	110000	15	CP000230_29	Continuation (30 o
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c	45	2035.5	49.5	110000	15	AP007255_33	Continuation (34 o

ALIGNMENTS

RESULT 1

BD236814

LOCUS BD236814 2475 bp DNA linear PAT 17-JUL-2003

DEFINITION Nucleic acid molecule encoding branching enzyme from *Neisseria* bacteria and process for producing alpha-1,6-branched alpha-1,4-glucane.

ACCESSION BD236814

VERSION BD236814.1 GI:33046584

KEYWORDS JP 2002527068-A/1.

SOURCE *Bergeriella denitrificans*ORGANISM *Bergeriella denitrificans*Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; *Bergeriella*.

REFERENCE 1 (bases 1 to 2475)

AUTHORS Buttcher,V. and Quanz,M.

TITLE Nucleic acid molecule encoding branching enzyme from *Neisseria* bacteria and process for producing alpha-1,6-branchedJOURNAL Patent: JP 2002527068-A 1 27-AUG-2002;
PLANTTEC BIOTECHNOLOGIE GMBH FORSCHUNG UND ENTWICKLUNG, MAX PLANCK
GESELLSCHAFT ZUR FOERDERUNG DER WISSENSCHAFTEN EVCOMMENT OS *Neisseria denitrificans*

PN JP 2002527068-A/1

PD 27-AUG-2002

PF 08-OCT-1999 JP 2000576030

PR 09-OCT-1998 DE 198 46 635.8,27-MAY-1999 DE 199 24 342.5 PI

VOLKER BUTTCHER,MARTIN QUANZ.

PC C12N15/09,A01H5/00,C07K16/40,C12N1/15,C12N1/19,C12N1/21,C12N5/

PC 10,C12N9/10,

PC C12P19/04,C12N15/00,C12N5/00

CC Nucleic acid molecule encoding branching
enzyme from *Neisseria*

CC bacteria

CC and process for producing alpha-1,6-branched alpha-1,4-glucane

FH Key Location/Qualifiers

FT CDS (170)..(2458).

FEATURES Location/Qualifiers

source 1..2475

/organism="*Bergeriella denitrificans*"

/mol_type="genomic DNA"

/db_xref="taxon:494"

ORIGIN

Alignment Scores:

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Score:	4112.00	Matches:	762
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	2	Gaps:	0

US-10-705-195-2 (1-762) x BD236814 (1-2475)

Qy 1 MetAsnArgAsnArgHisIleArgArgGlyTyrHisProGluAlaGlyGluArgGlnIle 20

Db	170	 ATGAACCGAAACCGCCATATCCGACGCGGCTACCACCCGGAAGCCGGAGAACGCCAAATC	229
Qy	21	IleAspSerLeuPheAlaAlaThrHisSerAspProPheAlaTyrLeuGlyArgHisArg	40
Db	230	 ATCGACAGCCTGTTTGCCGCCACCCACAGCGATCCGTTTGCCTATCTTGGGCGGCATCGT	289
Qy	41	ValAsnAspGluArgGluAlaValArgValLeuArgProAspAlaHisHisIleAspIle	60
Db	290	 GTCAACGACGAACGCGAAGCCGTGCGCGTGCTGCGTCCCGACGCGCACCACATCGACATC	349
Qy	61	IleAspArgHisThrGlyAlaValIleMetProSerGluLysIleAspGluArgGlyLeu	80
Db	350	 ATCGACCGCCACACAGGCGCAGTCATCATGCCGTCTGAAAAATCGACGAGCGCGGCCTG	409
Qy	81	PheAlaAlaValLeuProGluHisAlaProAspTyrAlaLeuLeuValThrTyrHisGlu	100
Db	410	 TTTGCCGCCGTATTGCCCGAACACGCGCCCGACTACGCCCTGCTGGTGACATACCACGAG	469
Qy	101	GlyGluAlaAlaValArgGluGluAspAspTyrArgPheGlySerAlaLeuGlnHisThr	120
Db	470	 GGCGAAGCCGCCGTACGCGAAGAAGATGACTACCGCTTCGGCAGCGCGCTGCAACATACC	529
Qy	121	AspAlaTrpLeuLeuGlyGluGlyThrHisLeuArgProTyrGluThrLeuGlyAlaHis	140
Db	530	 GATGCCTGGCTGCTGGGCGAAGGCACGCACCTGCGCCCTTATGAAACGCTGGGCGCACAT	589
Qy	141	PheAlaGluMetAspGlyValSerGlyValArgPheAlaValTrpAlaProAsnAlaArg	160
Db	590	 TTCGCCGAAATGGACGGCGTATCCGGCGTGCGCTTTGCCGTTTGGGCGCCCAACGCGCGG	649
Qy	161	ArgValSerValIleGlyGluPheAsnGlyTrpAspSerArgArgHisAlaMetArgPro	180
Db	650	 CGGGTATCGGTCATCGGCGAATTCAACGGCTGGGACAGCCGCCCGCCATGCCATGCGTCCG	709
Qy	181	HisThrGlyAsnGlyLeuTrpAspIlePheIleProGlyValGlyLeuAsnAlaLeuTyr	200
Db	710	 CACACAGGCAACGGCCTGTGGGACATCTTTATCCCCGGCGTCGGCCTCAACGCGCTGTAT	769
Qy	201	LysPheSerValLeuAspAlaAsnGlyAsnIleArgGluLysAlaAspProTyrAlaPhe	220
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Qy	221	GlyAlaGluLeuArgProThrThrAlaSerValValArgGlyLeuProAlaLysAlaGlu	240
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Qy	241	AlaProAlaPheArgArgArgAlaAsnSerValGluAlaProIleSerIleTyrGluVal	260
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Qy	261	HisLeuGlySerTrpArgArgAsnProGluAsnAsnTyrTrpLeuThrTyrThrGlnLeu	280
Db	950	 CATCTCGGCTCGTGGCGGCGCAATCCCGAAAAACAATACTGGGCTCACTACACGCAGCTG	1009
Qy	281	AlaAspGluLeuValAsnTyrValLysAspMetGlyPheThrHisIleGluLeuLeuPro	300
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Qy	301	LeuSerGluTyrProPheAspGlySerTrpGlyTyrGlnAlaThrGlyLeuTyrAlaPro	320

SCORE Search Results Details for Application 107 Search Result us-10-705-195-2.p2n.rng

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GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2006, 19:33:36 ; Search time 1177 Seconds
(without alignments)
6770.841 Million cell updates/sec

Title: US-10-705-195-2
Perfect score: 4112
Sequence: 1 MNRNRHIRRGYHPEAGERQI.....QTALRADKQPAVKDKQAKAK 762

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	2531	61.6	349980	13	ADT05737	Adt05737 Haemophil
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	5	2523	61.4	2193	8	ACA34445	Aca34445 Prokaryot
c	6	2481.5	60.3	6306	13	ADT05474	Adt05474 Haemophil
	7	2462.5	59.9	2361	2	AAV70952	Aav70952 DNA seque
	8	2462	59.9	2187	13	ADT48837	Adt48837 Bacterial
	9	2038.5	49.6	2164	13	ADT46098	Adt46098 Bacterial
	10	1996	48.5	2151	13	ADS55782	Ads55782 Bacterial
	11	1957.5	47.6	2148	13	ADT46962	Adt46962 Bacterial
	12	1939	47.2	2079	5	AAS88840	Aas88840 DNA encod
	13	1925.5	46.8	2154	13	ADS63589	Ads63589 Bacterial
	14	1925.5	46.8	2160	13	ADS63965	Ads63965 Bacterial
	15	1925.5	46.8	2160	13	ADT41565	Adt41565 Bacterial
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	17	1899.5	46.2	2214	13	ADS60312	Ads60312 Bacterial
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	19	1859	45.2	2199	13	ADS14563	Ads14563 Pseudomon
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	21	1828.5	44.5	2142	13	ADS63957	Ads63957 Bacterial
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	23	1828.5	44.5	2142	13	ADS63584	Ads63584 Bacterial
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	26	1805	43.9	2172	14	ACL68441	Acl68441 M. xanthu
	27	1805	43.9	2205	13	ADT44556	Adt44556 Bacterial
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	33	1746.5	42.5	2313	13	ADS48037	Ads48037 Bacterial
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c	35	1727	42.0	110000	4	AAI99683_14	Continuation (15 o
	36	1700	41.3	1893	10	ADC23310	Adc23310 DNA of Aq
	37	1700	41.3	1893	13	ADS45307	Ads45307 Bacterial
	38	1684	41.0	2268	13	ADT46200	Adt46200 Bacterial
	39	1657.5	40.3	22934	4	AAS59613	Aas59613 Propionib
	40	1657.5	40.3	22934	8	ACF64542	Acf64542 Propionib
	41	1649	40.1	349980	6	ABQ81846	Abq81846 Bifidobac

42	1649	40.1	349980	6	ABQ81847	Abq81847 Bifidobac
43	1626.5	39.6	2193	5	AAH66319	Aah66319 C glutami
44	1626.5	39.6	2316	4	AAF71540	Aaf71540 Corynebac
c 45	1626.5	39.6	349980	5	AAH68528	Aah68528 C glutami

ALIGNMENTS

RESULT 1

AAA11731

ID AAA11731 standard; DNA; 2475 BP.

XX

AC AAA11731;

XX

DT 21-JUL-2000 (first entry)

XX

DE N. denitrificans alpha-1,6-branched alpha-1,4 glucan DNA.

XX

KW Alpha-1,6-branched alpha-1,4-glucan; branching enzyme; binder; carrier;
 KW transgenic plant; flavor; perfume; packaging material; papermaking;
 KW ultra-violet light adsorber; starch; textile; wetting agent; ds.

XX

OS Neisseria denitrificans.

XX

FH Key Location/Qualifiers

FT CDS 170. .2458

FT /*tag= a

FT /product= "alpha-1,6-branched alpha-1,4-glucan"

XX

PN WO200022140-A1.

XX

PD 20-APR-2000.

XX

PF 08-OCT-1999; 99WO-EP007562.

XX

PR 09-OCT-1998; 98DE-01046635.

PR 27-MAY-1999; 99DE-01024342.

XX

PA (PLAN-) PLANTTEC BIOTECHNOLOGIE GMBH.

PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX

PI Buettcher V, Quanz M;

XX

DR WPI; 2000-317992/27.

DR P-PSDB; AAW90977.

XX

PT New nucleic acid encoding a branching enzyme, useful for in vitro
 PT synthesis of branched glucans and to prepare transgenic plants producing
 PT modified starch.

XX

PS Claim 1b; Page 93-96; 115pp; German.

XX

CC This invention describes a novel nucleic acid (I) isolated from Neisseria
 CC which encodes a branching enzyme (II). (I) is used for recombinant
 CC production of (II) subsequently used in the in vitro production of alpha-
 CC 1,6-branched alpha-1,4-glucans. It is also used to prepare transgenic
 CC plants that produce starches with modified properties. (III) are used as
 CC binders for tablets, carriers for pharmaceuticals, flavors and perfumes
 CC and powdered additives, packaging materials, ultra-violet light adsorbers
 CC in sunscreens and also for any of the usual applications of starch in
 CC foods, papermaking, as textile size, in soil stabilization, as wetting

CC agent for agricultural chemicals, as polymer additives etc. Fragments of
 CC (I) are useful as PCR primers and antisense molecules or ribozymes for
 CC inhibiting expression of (I), and the regulatory region of (II) can be
 CC used to control expression of heterologous sequences in host cells. (I)
 CC provides an inexpensive method for producing alpha-1,6-branched alpha-1,4
 CC -glucans (III), producing products that can be tailored for particular
 CC applications, particularly by controlling the degree of branching. Starch
 CC from transgenic plants has increased gel strength; reduced phosphate
 CC content; reduced peak viscosity; lower pasting temperature and granule
 CC size and/or altered sidechain distribution. This sequence encodes an
 CC alpha-1,6-branched alpha-1,4-glucan isolated from *Neisseria denitrificans*
 CC which is described in the method of the invention

XX

SQ Sequence 2475 BP; 560 A; 827 C; 674 G; 414 T; 0 U; 0 Other;

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US-10-705-195-2. (1-762) x AAA11731 (1-2475)

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Qy	101	GlyGluAlaAlaValArgGluGluAspAspTyrArgPheGlySerAlaLeuGlnHisThr	120
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Qy	121	AspAlaTrpLeuLeuGlyGluGlyThrHisLeuArgProTyrGluThrLeuGlyAlaHis	140
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SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-2.p2n.rni

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2006, 19:40:37 ; Search time 360 Seconds
(without alignments)
5940.770 Million cell updates/sec

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Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	5	2526	61.4	1830121	3	US-09-643-990A-1		Sequence 1, Appli
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c	11	1727	42.0	4403765	3	US-09-103-840A-2		Sequence 2, Appli
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ALIGNMENTS

RESULT 1

US-09-579-365-1

; Sequence 1, Application US/09579365

; Patent No. 6566585

; GENERAL INFORMATION:

; APPLICANT: Martin QUANZ

; TITLE OF INVENTION: GENETICALLY MODIFIED PLANT CELLS AND PLANTS WITH AN

; TITLE OF INVENTION: INCREASED ACTIVITY OF AN AMYLOSUCRASE PROTEIN AND A

; TITLE OF INVENTION: BRANCHING ENZYME

; FILE REFERENCE: 0147-0200P

; CURRENT APPLICATION NUMBER: US/09/579,365

; CURRENT FILING DATE: 2000-05-25

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2475

; TYPE: DNA

; ORGANISM: Neisseria denitrificans

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (170)..(2458)

US-09-579-365-1

Alignment Scores:

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Score:	4112.00	Matches:	762
Percent Similarity:	100.0%	Conservative:	0
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US-10-705-195-2 (1-762) x US-09-579-365-1 (1-2475)

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2006, 19:56:13 ; Search time 495 Seconds
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Listing first 45 summaries

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SUMMARIES

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	3	1224.5	29.8	1869	9	US-11-348-413-6911	Sequence 6911, Ap
	4	618.5	15.0	2668	9	US-11-056-355B-76595	Sequence 76595, A
	5	614.5	14.9	2763	9	US-11-056-355B-99154	Sequence 99154, A
	6	614.5	14.9	2763	9	US-11-056-355B-110393	Sequence 110393,
	7	614.5	14.9	2764	6	US-10-953-349-4536	Sequence 4536, Ap
	8	614.5	14.9	2764	9	US-11-056-355B-27071	Sequence 27071, A
	9	614.5	14.9	2764	9	US-11-056-355B-30239	Sequence 30239, A
	10	614.5	14.9	2764	9	US-11-056-355B-33829	Sequence 33829, A
	11	604.5	14.7	3643	8	US-11-216-545-3261	Sequence 3261, Ap
	12	598	14.5	2588	9	US-11-056-355B-100250	Sequence 100250,
	13	598	14.5	2588	9	US-11-056-355B-111489	Sequence 111489,
	14	593	14.4	2759	9	US-11-218-305-12548	Sequence 12548, A
	15	592.5	14.4	2763	9	US-11-056-355B-19641	Sequence 19641, A
	16	592.5	14.4	2763	9	US-11-056-355B-19806	Sequence 19806, A
	17	592.5	14.4	2826	9	US-11-218-305-12549	Sequence 12549, A
	18	587	14.3	2640	9	US-11-330-822-58	Sequence 58, Appl
	19	569	13.8	3553	6	US-10-449-902-12839	Sequence 12839, A
	20	566	13.8	2649	6	US-10-539-723-6	Sequence 6, Appli
	21	547.5	13.3	2763	9	US-11-330-822-60	Sequence 60, Appl
	22	547.5	13.3	2790	9	US-11-056-355B-11438	Sequence 11438, A
	23	547.5	13.3	3022	9	US-11-218-305-9897	Sequence 9897, Ap
	24	539	13.1	2891	8	US-11-266-748A-25857	Sequence 25857, A
	25	530.5	12.9	3827	6	US-10-449-902-18529	Sequence 18529, A
	26	528.5	12.9	2729	6	US-10-449-902-14548	Sequence 14548, A
	27	511.5	12.4	2115	8	US-11-217-529-698	Sequence 698, App
	28	500	12.2	2115	8	US-11-217-529-76256	Sequence 76256, A
	29	450	10.9	3290	6	US-10-449-902-16439	Sequence 16439, A
	30	442	10.7	1641	6	US-10-539-723-4	Sequence 4, Appli
	31	404	9.8	15294	6	US-10-547-660-15	Sequence 15, Appl
	32	330.5	8.0	640	8	US-11-266-748A-119619	Sequence 119619,
c	33	330.5	8.0	641	8	US-11-266-748A-81241	Sequence 81241, A
	34	330.5	8.0	641	8	US-11-266-748A-134052	Sequence 134052,
	35	320.5	7.8	1118	8	US-11-266-748A-228183	Sequence 228183,
	36	247	6.0	1338	9	US-11-316-535A-21	Sequence 21, Appl
	37	239	5.8	1974	9	US-11-275-569-15	Sequence 15, Appl
	38	231.5	5.6	4079	9	US-11-218-305-206	Sequence 206, App
	39	216	5.3	2301	9	US-11-348-413-6910	Sequence 6910, Ap
	40	213	5.2	1323	9	US-11-316-535A-39	Sequence 39, Appl
	41	209	5.1	1749	9	US-11-316-535A-178	Sequence 178, App
	42	201	4.9	1353	9	US-11-316-535A-122	Sequence 122, App
	43	199	4.8	1704	9	US-11-348-413-4882	Sequence 4882, Ap
	44	198.5	4.8	1202	8	US-11-266-748A-8695	Sequence 8695, Ap

Db	193	TCACGGGGATTCTTTAGCGGCGTCATTCCGCGACGTAAGAATTTTTTCCGCTATCAGTTG	252
Qy	95	LeuValThrTyrHisGluGlyGluAlaAlaValArgGluGluAspAspTyrArgPheGly	114
Db	253	GCTGTTGTCTGGCATGGTCAGCAAAACCTGATT-----GATGATCCTTACCGTTTTGGT	306
Qy	115	SerAlaLeuGlnHisThrAspAlaTrpLeuLeuGlyGluGlyThrHisLeuArgProTyr	134
Db	307	CCGCTAATCCAGGAAATGGATGCCTGGCTATTATCTGAAGGTACTCACCTGCGCCCGTAT	366
Qy	135	GluThrLeuGlyAlaHisPheAlaGluMetAspGlyValSerGlyValArgPheAlaVal	154
Db	367	GAAACCTTAGGCGCGCATGCAGATACTATGGATGGCGTCACAGGTACGCGTTTCTCTGTC	426
Qy	155	TrpAlaProAsnAlaArgArgValSerValIleGlyGluPheAsnGlyTrpAspSerArg	174
Db	427	TGGGCTCCAAACGCCCGTCGGGTCTCGGTGGTGGGCAATTCAACTACTGGGACGGTCGC	486
Qy	175	ArgHisAlaMetArgProHisThrGlyAsnGlyLeuTrpAspIlePheIleProGlyVal	194
Db	487	CGTCACCCGATGCGCCTGCGTAAAGAGAGCGGCATCTGGGAAGTGTATCCCTGGGGCG	546
Qy	195	GlyLeuAsnAlaLeuTyrLysPheSerValLeuAspAlaAsnGlyAsnIleArgGluLys	214
Db	547	CATAACGGTCAGCTCTATAAATACGAGATGATTGATGCCAATGGCAACTTGCCTCTGAAG	606
Qy	215	AlaAspProTyrAlaPheGlyAlaGluLeuArgProThrThrAlaSerValValArgGly	234
Db	607	TCCGACCCTTATGCCTTTGAAGCGCAAATGCGCCCGAAACCGCGTCTCTTATTTGCGGG	666
Qy	235	LeuProAlaLysAlaGluAlaProAlaPheArgArgArgAlaAsnSerValGluAlaPro	254
Db	667	CTGCCGAAAAGGTTGTACAGACTGAAGAGCGCAAAAAGCGAATCAGTTTGATGCGCCA	726
Qy	255	IleSerIleTyrGluValHisLeuGlySerTrpArgArgAsnProGluAsnAsnTyrTrp	274
Db	727	ATCTCTATTTATGAAGTTCACCTGGGTTCCTGGCGTCGCCACACCGACAACAATTTCTGG	786
Qy	275	LeuThrTyrThrGlnLeuAlaAspGluLeuValAsnTyrValLysAspMetGlyPheThr	294
Db	787	TTGAGCTACCGCGAGCTGGCCGATCAACTGGTGCCTTATGCTAAATGGATGGGCTTTACC	846
Qy	295	HisIleGluLeuLeuProLeuSerGluTyrProPheAspGlySerTrpGlyTyrGlnAla	314
Db	847	CACCTCGAACTACTGCCCATTAAACGAGCATCCCTTCGATGGCAGTTGGGGTTATCAGCCA	906
Qy	315	ThrGlyLeuTyrAlaProThrSerArgPheGlySerProAspGluLeuLysAlaLeuIle	334
Db	907	ACCGGCCTGTATGCGCCAACCCGCCGTTTTGGTACTCGCGACGACTTCCGTTATTTTCATT	966
Qy	335	AspAlaAlaHisAlaAlaGlyIleSerValIleLeuAspTrpValAlaGlyHisPhePro	354
Db	967	GATGCCGACACGCAGCTGGTCTGAACGTGATTCTCGACTGGGTGCCAGGCCACTTCCCG	1026
Qy	355	ThrAspAspHisGlyLeuAsnThrPheAspGlyThrAlaLeuTyrGluHisAlaAspPro	374
Db	1027	ACTGATGACTTTGCGCTTGCCGAATTTGATGGCACGAACCTGTATGAACACAGCGATCCG	1086
Qy	375	ArgGluGlyTyrHisGlnAspTrpAsnThrLeuIleTyrAsnPheGlyArgAsnGluVal	394

SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-2.p2n.rnpbn

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OM protein - nucleic search, using frame_plus_p2n model

Run on: August 22, 2006, 19:56:13 ; Search time 495 Seconds
(without alignments)
3691.235 Million cell updates/sec

Title: US-10-705-195-2
Perfect score: 4112
Sequence: 1 MNRNRHIRRGYHPEAGERQI.....QTALRADKQPAVKDKQAKAK 762

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss04
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
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3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*

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 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB				Description
	Score	Match Length	ID				
1	2462.5	59.9	2361	9	US-11-330-822-38		Sequence 38, Appl
2	2462	59.9	2187	9	US-11-275-569-17		Sequence 17, Appl
3	1224.5	29.8	1869	9	US-11-348-413-6911		Sequence 6911, Ap
4	618.5	15.0	2668	9	US-11-056-355B-76595		Sequence 76595, A
5	614.5	14.9	2763	9	US-11-056-355B-99154		Sequence 99154, A
6	614.5	14.9	2763	9	US-11-056-355B-110393		Sequence 110393,
7	614.5	14.9	2764	6	US-10-953-349-4536		Sequence 4536, Ap
8	614.5	14.9	2764	9	US-11-056-355B-27071		Sequence 27071, A
9	614.5	14.9	2764	9	US-11-056-355B-30239		Sequence 30239, A
10	614.5	14.9	2764	9	US-11-056-355B-33829		Sequence 33829, A
11	604.5	14.7	3643	8	US-11-216-545-3261		Sequence 3261, Ap
12	598	14.5	2588	9	US-11-056-355B-100250		Sequence 100250,
13	598	14.5	2588	9	US-11-056-355B-111489		Sequence 111489,
14	593	14.4	2759	9	US-11-218-305-12548		Sequence 12548, A
15	592.5	14.4	2763	9	US-11-056-355B-19641		Sequence 19641, A
16	592.5	14.4	2763	9	US-11-056-355B-19806		Sequence 19806, A
17	592.5	14.4	2826	9	US-11-218-305-12549		Sequence 12549, A
18	587	14.3	2640	9	US-11-330-822-58		Sequence 58, Appl
19	569	13.8	3553	6	US-10-449-902-12839		Sequence 12839, A
20	566	13.8	2649	6	US-10-539-723-6		Sequence 6, Appli
21	547.5	13.3	2763	9	US-11-330-822-60		Sequence 60, Appl
22	547.5	13.3	2790	9	US-11-056-355B-11438		Sequence 11438, A
23	547.5	13.3	3022	9	US-11-218-305-9897		Sequence 9897, Ap
24	539	13.1	2891	8	US-11-266-748A-25857		Sequence 25857, A
25	530.5	12.9	3827	6	US-10-449-902-18529		Sequence 18529, A
26	528.5	12.9	2729	6	US-10-449-902-14548		Sequence 14548, A
27	511.5	12.4	2115	8	US-11-217-529-698		Sequence 698, App
28	500	12.2	2115	8	US-11-217-529-76256		Sequence 76256, A
29	450	10.9	3290	6	US-10-449-902-16439		Sequence 16439, A
30	442	10.7	1641	6	US-10-539-723-4		Sequence 4, Appli
31	404	9.8	15294	6	US-10-547-660-15		Sequence 15, Appl
32	330.5	8.0	640	8	US-11-266-748A-119619		Sequence 119619,
c 33	330.5	8.0	641	8	US-11-266-748A-81241		Sequence 81241, A
34	330.5	8.0	641	8	US-11-266-748A-134052		Sequence 134052,
35	320.5	7.8	1118	8	US-11-266-748A-228183		Sequence 228183,
36	247	6.0	1338	9	US-11-316-535A-21		Sequence 21, Appl
37	239	5.8	1974	9	US-11-275-569-15		Sequence 15, Appl
38	231.5	5.6	4079	9	US-11-218-305-206		Sequence 206, App
39	216	5.3	2301	9	US-11-348-413-6910		Sequence 6910, Ap
40	213	5.2	1323	9	US-11-316-535A-39		Sequence 39, Appl
41	209	5.1	1749	9	US-11-316-535A-178		Sequence 178, App
42	201	4.9	1353	9	US-11-316-535A-122		Sequence 122, App
43	199	4.8	1704	9	US-11-348-413-4882		Sequence 4882, Ap
44	198.5	4.8	1202	8	US-11-266-748A-8695		Sequence 8695, Ap

Db	193	TCACGGGGATTCTTTAGCGGCGTCATTCCGCGACGTAAGAATTTTTTCCGCTATCAGTTG	252						
Qy	95	LeuValThrTyrHisGluGlyGluAlaAlaValArgGluGluAspAspTyrArgPheGly	114						
Db	253	GCTGTTGTCTGGCATGGTCAGCAAAACCTGATT-----GATGATCCTTACCGTTTGTGT	306						
Qy	115	SerAlaLeuGlnHisThrAspAlaTrpLeuLeuGlyGluGlyThrHisLeuArgProTyr	134						
Db	307	CCGCTAATCCAGGAAATGGATGCCTGGCTATTATCTGAAGGTACTCACCTGCGCCCGTAT	366						
Qy	135	GluThrLeuGlyAlaHisPheAlaGluMetAspGlyValSerGlyValArgPheAlaVal	154						
Db	367	GAAACCTTAGGCGCGCATGCAGATACTATGGATGGCGTCACAGGTACGCGTTTCTCTGTC	426						
Qy	155	TrpAlaProAsnAlaArgArgValSerValIleGlyGluPheAsnGlyTrpAspSerArg	174						
Db	427	TGGGCTCCAAACGCCCGTCGGGTCTCGGTGGTTGGGCAATTCAACTACTGGGACGGTCGC	486						
Qy	175	ArgHisAlaMetArgProHisThrGlyAsnGlyLeuTrpAspIlePheIleProGlyVal	194						
Db	487	CGTCACCCGATGCGCCTGCGTAAAGAGAGCGGCATCTGGGAAGTGTATCCCTGGGGCG	546						
Qy	195	GlyLeuAsnAlaLeuTyrLysPheSerValLeuAspAlaAsnGlyAsnIleArgGluLys	214						
Db	547	CATAACGGTCAGCTCTATAAATACGAGATGATTGATGCCAATGGCAACTTGCCTCTGAAG	606						
Qy	215	AlaAspProTyrAlaPheGlyAlaGluLeuArgProThrThrAlaSerValValArgGly	234						
Db	607	TCCGACCCTTATGCCTTTGAAGCGCAAATGCGCCCGAAACCGCGTCTCTTATTTGCGGG	666						
Qy	235	LeuProAlaLysAlaGluAlaProAlaPheArgArgArgAlaAsnSerValGluAlaPro	254						
Db	667	CTGCCGGAAGGTTGTACAGACTGAAGAGCGCAAAAAGCGAATCAGTTTGATGCGCCA	726						
Qy	255	IleSerIleTyrGluValHisLeuGlySerTrpArgArgAsnProGluAsnAsnTyrTrp	274						
Db	727	ATCTCTATTTATGAAGTTCACCTGGGTTCTGGCGTCGCCACACCGACAACAATTCTGG	786						
Qy	275	LeuThrTyrThrGlnLeuAlaAspGluLeuValAsnTyrValLysAspMetGlyPheThr	294						
Db	787	TTGAGCTACCGCGAGCTGGCCGATCAACTGGTGCCTTATGCTAAATGGATGGGCTTACC	846						
Qy	295	HisIleGluLeuLeuProLeuSerGluTyrProPheAspGlySerTrpGlyTyrGlnAla	314						
Db	847	CACCTCGAACTACTGCCATTAAACGAGCATCCCTTCGATGGCAGTTGGGGTTATCAGCCA	906						
Qy	315	ThrGlyLeuTyrAlaProThrSerArgPheGlySerProAspGluLeuLysAlaLeuIle	334						
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Qy	335	AspAlaAlaHisAlaAlaGlyIleSerValIleLeuAspTrpValAlaGlyHisPhePro	354						
Db	967	GATGCCGCACACGCAGCTGGTCTGAACGTGATTCTGACTGGGTGCCAGGCCACTTCCCG	1026						
Qy	355	ThrAspAspHisGlyLeuAsnThrPheAspGlyThrAlaLeuTyrGluHisAlaAspPro	374						
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Qy	375	ArgGluGlyTyrHisGlnAspTrpAsnThrLeuIleTyrAsnPheGlyArgAsnGluVal	394						

SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-2.p2n.rst.

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OM protein - nucleic search, using frame plus p2n model

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Run on:      August 22, 2006, 19:37:06 ; Search time 8926 Seconds
              (without alignments)
              7160.631 Million cell updates/sec
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Perfect score:  4112
Sequence:       1 MNRNRHIRRGYHPEAGERQI.....QTALRADKQPAVKDKQAKAK 762
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                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop  6.0 , Fgapext 7.0
                  Delop  6.0 , Delext 7.0
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Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Command line parameters:
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-Q=/abss/ABSSWEB_spool/US10705195/runat_22082006_095551_883/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss08
-USER=US10705195_@CGN_1_1_6323_@runat_22082006_095551_883 -NCPU=6 -ICPU=3
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

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Database :      EST:*
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 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_gss1:*
 12: gb_gss2:*
 13: gb_gss3:*
 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB			
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c	2	1075	26.1	1342	12	CG755637	CG755637	P051-1-G0
	3	947.5	23.0	1003	14	DU773085	DU773085	APKG3284.
	4	919	22.3	922	14	DU787945	DU787945	APKH2378.
c	5	881.5	21.4	1008	14	DU785952	DU785952	APKH1378.
	6	756	18.4	1035	14	DU743159	DU743159	ASNC1588.
c	7	738.5	18.0	1161	12	CG752267	CG752267	P046-4-G1
	8	729.5	17.7	1163	12	BZ569819	BZ569819	msh2_1033
	9	715	17.4	634	13	CL675608	CL675608	PRI0115b_
	10	669	16.3	528	13	CL667597	CL667597	PRI0155c_
	11	661	16.1	732	12	CG410928	CG410928	RM1062 Lx
	12	656	16.0	584	1	AJ879817	AJ879817	AJ879817
	13	652	15.9	1060	11	BZ557122	BZ557122	pacs1-60_
c	14	623	15.2	543	11	BH783525	BH783525	fzmb013f0
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	19	553	13.4	2766	6	AY109521	AY109521	Zea mays
	20	550	13.4	417	14	DX059445	DX059445	KBrB065F1
	21	547	13.3	2738	6	AK009815	AK009815	Mus muscu
	22	547	13.3	2862	6	AK050365	AK050365	Mus muscu
	23	535.5	13.0	3012	6	AY105679	AY105679	Zea mays
	24	532	12.9	443	5	CK339918	CK339918	C0871G07-
	25	514.5	12.5	3305	6	AK050423	AK050423	Mus muscu
	26	504	12.3	2732	6	AY109532	AY109532	Zea mays
	27	495	12.0	2044	14	AY413117	AY413117	Mus muscu
c	28	493	12.0	1569	12	CG755635	CG755635	P051-1-G0
	29	492.5	12.0	717	1	AJ797306	AJ797306	AJ797306
	30	474	11.5	2109	14	AY413115	AY413115	Homo sapi
	31	474	11.5	2109	14	AY413116	AY413116	Pan trogl
	32	470.5	11.4	1275	6	AY811197	AY811197	Schistoso
c	33	470.5	11.4	1482	11	BH770747	BH770747	LLMtag49
	34	451	11.0	504	12	CG411053	CG411053	RM367 Lxx
c	35	442.5	10.8	609	12	CG411057	CG411057	RM372 Lxx
c	36	429.5	10.4	439	12	CG411069	CG411069	RM384 Lxx
c	37	418	10.2	1317	12	BZ572034	BZ572034	msh2_240.
	38	417.5	10.2	852	5	CD438018	CD438018	EL01N0508

39	401	9.8	316	5	CK339021	CK339021 C0821D11-
40	396.5	9.6	1167	5	CD664476	CD664476 TVEST020.
41	393.5	9.6	825	8	CO467539	CO467539 MZCCL2004
42	388.5	9.4	843	8	CO098553	CO098553 GR_Ea22P
43	379.5	9.2	906	8	CO456486	CO456486 MZCCL2000
44	377	9.2	1411	10	DT989097	DT989097 CLJ241-E0
45	375	9.1	706	5	CF638461	CF638461 D02_H06 F

ALIGNMENTS

RESULT 1

CG755636/c

LOCUS CG755636 1261 bp DNA linear GSS 24-OCT-2003

DEFINITION P051-1-G03.yb Ppa EcoRI BAC Library *Pristionchus pacificus* genomic, genomic survey sequence.

ACCESSION CG755636

VERSION CG755636.1 GI:37982332

KEYWORDS GSS.

SOURCE *Pristionchus pacificus*ORGANISM *Pristionchus pacificus*Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; *Pristionchus*.

REFERENCE 1 (bases 1 to 1261)

AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.TITLE An integrated physical and genetic map of the nematode *Pristionchus pacificus*

JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)

PUBMED 12884007

COMMENT Contact: Sommer RJ

Evolutionary Biology

Max-Planck-Institute for Developmental Biology

Spemannstr. 37-39, Tuebingen D-72076, Germany

Tel: 00497071601371

Fax: 00497071601498

Email: ralf.sommer@tuebingen.mpg.de

Class: BAC ends.

FEATURES

Location/Qualifiers

source

1. .1261

/organism="*Pristionchus pacificus*"

/mol_type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone_lib="Ppa EcoRI BAC Library"

/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

ORIGIN

Alignment Scores:

Pred. No.:	3.18e-115	Length:	1261
Score:	1159.50	Matches:	218
Percent Similarity:	79.6%	Conservative:	40
Best Local Similarity:	67.3%	Mismatches:	60
Query Match:	28.2%	Indels:	6
DB:	12	Gaps:	2

US-10-705-195-2 (1-762) x CG755636 (1-1261)

Qy 133 ProTyrGluThrLeuGlyAlaHisPheAlaGlu-----MetAspGlyValSerGlyVal 150

Db	1050					991
Qy	151	Arg---PheAlaVal-TrpAlaProAsnAlaArg-ArgValSerValIleGlyGluPheA	169			
Db	990	CGCGTTTTCTCTGTTTTGGGCTCCAAACGCCCGTTCGGGTCTCGGTGGTGGGCAATTCA	931			
Qy	169	snGlyTrpAspSerArgArgHisAlaMetArgProHisThrGlyAsnGlyLeuTrpAspI	189			
Db	930	ACTACTGGGACGGTCGCCGTACCCGATGCCCTGCGTAAAGAGAGCGGCATCTGGGAAC	871			
Qy	189	lePheIleProGlyValGlyLeuAsnAlaLeu-TyrLysPheSerValLeuAspAlaAsn	208			
Db	870	TGTTTATCCCTGGGGCGCATAACGGTCAGCTCTTATAAATACGAGATGATTGATGCCAAT	811			
Qy	209	GlyAsnIleArgGluLysAlaAspProTyrAlaPheGlyAlaGluLeuArgProThrThr	228			
Db	810	GGCAACTTGCGTCTGAAGTCCGACCCCTTATGCCTTCGAAGCGCAAATGCGCCCGAAACC	751			
Qy	229	AlaSerValValArgGlyLeuProAlaLysAlaGluAlaProAlaPheArgArgArgAla	248			
Db	750	GCGTCTCTTATTTGCGGGCTGCCGAAAAGGTTGTACAGACTGAAGAGCGCAAAAAGCG	691			
Qy	249	AsnSerValGluAlaProIleSerIleTyrGluValHisLeuGlySerTrpArgArgAsn	268			
Db	690	AATCAGTTTGATGCGCCAATCTCTATTTATGAAGTTCACCTGGGTTCCTGGCGTCGCCAC	631			
Qy	269	ProGluAsnAsnTyrTrpLeuThrTyrThrGlnLeuAlaAspGluLeuValAsnTyrVal	288			
Db	630	ACCGACAACAATTTCTGGTTGAGCTACCGCGAGCTGGCCGATCAACTGGTGCCTTATGCT	571			
Qy	289	LysAspMetGlyPheThrHisIleGluLeuLeuProLeuSerGluTyrProPheAspGly	308			
Db	570	AAATGGATGGGCTTTACCCACCTCGAACTACTGCCCATTAACGAGCATCCCTTCGATGGC	511			
Qy	309	SerTrpGlyTyrGlnAlaThrGlyLeuTyrAlaProThrSerArgPheGlySerProAsp	328			
Db	510	AGTTGGGGTTATCAGCCAACCGGCCTGTATGCACCAACCGCCGTTTTGGTACTCGCGAC	451			
Qy	329	GluLeuLysAlaLeuIleAspAlaAlaHisAlaAlaGlyIleSerValIleLeuAspTrp	348			
Db	450	GACTTCCGTTATTTTATTGATGCCGCACACGCAGCTGGTCTGAACGTGATTCTCGACTGG	391			
Qy	349	ValAlaGlyHisPheProThrAspAspHisGlyLeuAsnThrPheAspGlyThrAlaLeu	368			
Db	390	GTGCCAGGCCACTTCCCGACCGATGACTTTGCGCTTGCCGAATTTGATGGCAGCAACTTG	331			
Qy	369	TyrGluHisAlaAspProArgGluGlyTyrHisGlnAspTrpAsnThrLeuIleTyrAsn	388			
Db	330	TATGAACACAGCGATCCGCGTGAAGGCTATCATCAGGACTGGAACACGCTGATCTACAAC	271			
Qy	389	PheGlyArgAsnGluValLysAsnPheLeuGlnGlyAsnAlaLeuTyrTrpIleGluArg	408			
Db	270	TATGGTCGCCGTGAAGTCAGTAACTTCCTCGTCGGTAACGCGCTTTACTGGATTGAACGT	211			
Qy	409	PheGlyPheAspGlyIleArgValAspAlaValAlaSerMetIleTyrArgAsnTyrSer	428			
Db	210	TTTGGTATTGATGCGCTGCGCGTCGATGCGGTGCGGTCAATGATTTATCGCGACTACAGC	151			
Qy	429	ArgLysAspGlyGluTrpIleProAsnArgTyrGlyGlySerGluAsnLeuGluAlaIle	448			

SCORE Search Results Details for Application 10705195 and Search Result us-10-705-195-1.rst.

[Score Home](#) [Retrieve Application](#) [SCORE System](#) [SCORE](#) [Comments /](#)
[Page](#) [List](#) [Overview](#) [FAQ](#) [Suggestions](#)

This page gives you Search Results detail for the Application 10705195 and Search Result us-10-705-195-1.rst.

[start](#)

[Go Back to previous page](#)

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2006, 19:25:16 ; Search time 10532 Seconds
(without alignments)
13140.937 Million cell updates/sec

Title: US-10-705-195-1
Perfect score: 2475
Sequence: 1 actgtatgccgtgcagctgg.....taaagcggcaccatactgcc 2475

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est3:*
- 3: gb_est4:*
- 4: gb_est5:*
- 5: gb_est6:*
- 6: gb_htc:*
- 7: gb_est2:*
- 8: gb_est7:*
- 9: gb_est8:*
- 10: gb_est9:*
- 11: gb_gss1:*
- 12: gb_gss2:*
- 13: gb_gss3:*
- 14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
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	3	335.4	13.6	1003	14	DU773085	DU773085 APKG3284.
	4	302	12.2	922	14	DU787945	DU787945 APKH2378.
c	5	275.2	11.1	1161	12	CG752267	CG752267 P046-4-G1
	6	262	10.6	528	13	CL667597	CL667597 PRI0155c_
	7	260.8	10.5	1163	12	BZ569819	BZ569819 msh2_1033
	8	258.4	10.4	634	13	CL675608	CL675608 PRI0115b_
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	10	238.6	9.6	1060	11	BZ557122	BZ557122 pacs1-60_
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	13	210.6	8.5	417	14	DX059445	DX059445 KBrB065F1
	14	207.8	8.4	443	5	CK339918	CK339918 C0871G07-
c	15	203.4	8.2	605	12	CG411045	CG411045 RM359 Lxx
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	17	195.4	7.9	971	14	DU754880	DU754880 ASNF4137.
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c	19	187.6	7.6	1569	12	CG755635	CG755635 P051-1-G0
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c	21	158.2	6.4	609	12	CG411057	CG411057 RM372 Lxx
c	22	154.8	6.3	439	12	CG411069	CG411069 RM384 Lxx
	23	146.8	5.9	316	5	CK339021	CK339021 C0821D11-
	24	146.4	5.9	504	12	CG411053	CG411053 RM367 Lxx
	25	144.4	5.8	671	2	BI719233	BI719233 1031042C0
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	27	133.6	5.4	1035	14	DU743159	DU743159 ASNC1588.
c	28	133	5.4	320	8	CV983818	CV983818 UMC-bof_0
	29	130.8	5.3	663	5	CF638951	CF638951 D09_B01 F
	30	130.8	5.3	706	5	CF638461	CF638461 D02_H06 F
	31	113	4.6	950	10	DR638327	DR638327 EST102895
c	32	112.2	4.5	361	13	CZ443531	CZ443531 contig_RS
c	33	109	4.4	903	11	BZ554984	BZ554984 pacs1-60_
c	34	107.8	4.4	216	5	CK336186	CK336186 C0143B08-
c	35	106	4.3	1242	12	BZ572104	BZ572104 msh2_2516
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	42	99.4	4.0	747	8	CO568637	CO568637 AGENCOURT
	43	99.2	4.0	993	14	DU745819	DU745819 ASNC2988.
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ALIGNMENTS

RESULT 1

CG755636/c

LOCUS

CG755636

1261 bp

DNA

linear

GSS 24-OCT-2003

DEFINITION P051-1-G03.yb Ppa EcoRI BAC Library *Pristionchus pacificus* genomic, genomic survey sequence.

ACCESSION CG755636

VERSION CG755636.1 GI:37982332

KEYWORDS GSS.

SOURCE *Pristionchus pacificus*

ORGANISM *Pristionchus pacificus*
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; *Pristionchus*.

REFERENCE 1 (bases 1 to 1261)

AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.

TITLE An integrated physical and genetic map of the nematode *Pristionchus pacificus*

JOURNAL Mol. Genet. Genomics 269 (5), 715-722 (2003)

PUBMED 12884007

COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.

FEATURES Location/Qualifiers

source 1. .1261
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/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."

ORIGIN

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Best Local Similarity 67.4%; Pred. No. 1e-95;
Matches 623; Conservative 0; Mismatches 299; Indels 2; Gaps 2;

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Db      976 TTTGGGCTCAAACGCGCGTTCGGGTCTCGGTGGTTGGGCAATTCAACTACTGGGACGGT 917

Qy      689 CGCCGCCATGCCATGCGTCCGCACACAGGCAACGGCCTGTGGGACATCTTTATCCCCGGC 748
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RESULT 2

CG755637/c

LOCUS CG755637 1342 bp DNA linear GSS 24-OCT-2003

DEFINITION P051-1-G03.yc Ppa EcoRI BAC Library Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CG755637

VERSION CG755637.1 GI:37982334

KEYWORDS GSS.

SOURCE Pristionchus pacificus

ORGANISM Pristionchus pacificus

Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

REFERENCE 1 (bases 1 to 1342)

AUTHORS Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntjer,J., van der Meulen,M. and Sommer,R.J.TITLE An integrated physical and genetic map of the nematode Pristionchus
pacificus